

Ref#	Hits	Search Query	DBs	Default Operator	Plurals	Time Stamp
L1	716	southern with blot same bacter\$4 same detect\$4	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	ON	2005/05/05 10:43
L2	591	southern with blot same bacter\$4 same detect\$4 same pcr	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	ON	2005/05/05 10:43
L3	26	southern with blot same bacter\$4 same detect\$4 same pcr same sample	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	ON	2005/05/05 10:43



## Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

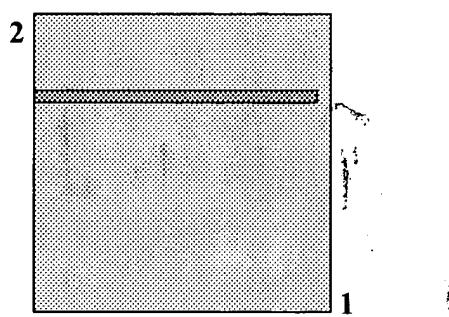
Structure

### BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.10 [Oct-19-2004]

Match: 1 Mismatch: -2 gap open: 5 gap extension: 2  
 x\_dropoff: 50 expect: 10.000 wordsize: 11  Filter  Align

Sequence 1 lcl|seq\_1 Length 20 (1 .. 20)

Sequence 2 gi 1799980 E.coli genomic DNA, Kohara clone #436(58.4-58.8 min.) Length 16446 (1 .. 16446)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

NOTE: If protein translation is reversed, please repeat the search with reverse strand of the query sequence

Score = 39.1 bits (20), Expect = 0.046

Identities = 20/20 (100%)

Strand = Plus / Minus

Query: 1 ttcgggttgtcatgccaatg 20  
 |||||||  
 Sbjct: 11799 ttcgggttgtcatgccaatg 11780 *yamamoto et al.*

*SEQ ID NO 2*

CPU time: 0.01 user secs. 0.00 sys. secs 0.01 total secs.

Lambda K H  
 1.33 0.621 1.12

Gapped Lambda K H  
 1.33 0.621 1.12

Matrix: blastn matrix:1 -2  
 Gap Penalties: Existence: 5, Extension: 2  
 Number of Sequences: 1  
 Number of Hits to DB: 5

Number of extensions: 1  
Number of successful extensions: 1  
Number of sequences better than 10.0: 1  
Number of HSP's better than 10.0 without gapping: 1  
Number of HSP's gapped: 1  
Number of HSP's successfully gapped: 1  
Number of extra gapped extensions for HSPs above 10.0: 0  
Length of query: 20  
Length of database: 13,936,275,478  
Length adjustment: 18  
Effective length of query: 2  
Effective length of database: 13,936,275,460  
Effective search space: 27872550920  
Effective search space used: 27872550920  
Neighboring words threshold: 0  
Window for multiple hits: 0  
X1: 11 (21.1 bits)  
X2: 26 (50.0 bits)  
X3: 26 (50.0 bits)  
S1: 12 (23.8 bits)  
S2: 16 (31.5 bits)



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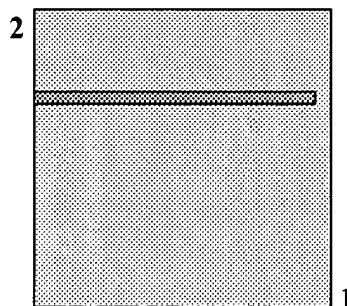
Structure

### BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.10 [Oct-19-2004]

Match: 1 Mismatch: -2 gap open: 5 gap extension: 2  
 x\_dropoff: 50 expect: 10.000 wordsize: 11  Filter  Align

**Sequence 1** lcl|seq\_1 **Length 18 (1 .. 18)**

**Sequence 2** gi 1799980 E.coli genomic DNA, Kohara clone #436(58.4-58.8 min.) **Length 16446 (1 .. 16446)**



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

NOTE: If protein translation is reversed, please repeat the search with reverse strand of the query sequence

Score = 35.3 bits (18), Expect = 0.66  
 Identities = 18/18 (100%)  
 Strand = Plus / Plus

Query: 1 ccgcccaggcaaattctgt 18 | SEQ ID NO 25  
 |||||||  
 Sbjct: 11482 ccgcccaggcaaattctgt 11499 yAMAMOTO et al.

CPU time: 0.01 user secs. 0.01 sys. secs 0.02 total secs.

Lambda K H  
 1.33 0.621 1.12

Gapped  
 Lambda K H  
 1.33 0.621 1.12

Matrix: blastn matrix:1 -2  
 Gap Penalties: Existence: 5, Extension: 2  
 Number of Sequences: 1  
 Number of Hits to DB: 4

Number of extensions: 1  
Number of successful extensions: 1  
Number of sequences better than 10.0: 1  
Number of HSP's better than 10.0 without gapping: 1  
Number of HSP's gapped: 1  
Number of HSP's successfully gapped: 1  
Number of extra gapped extensions for HSPs above 10.0: 0  
Length of query: 18  
Length of database: 13,936,275,478  
Length adjustment: 16  
Effective length of query: 2  
Effective length of database: 13,936,275,462  
Effective search space: 27872550924  
Effective search space used: 27872550924  
Neighboring words threshold: 0  
Window for multiple hits: 0  
X1: 11 (21.1 bits)  
X2: 26 (50.0 bits)  
X3: 26 (50.0 bits)  
S1: 12 (23.8 bits)  
S2: 16 (31.5 bits)